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The scores below are sorted by initi Significance is calculated based on
                                                         Number
Number
Number
                                                                                                    Times:
                                                                                                                                                                                                  Similarity matrix Mismatch penalty
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                                                                                                                                Scores:
                                                                                                                                                                          Gap size penalty Cutoff score
                                                                                                                                                                                           Gap Penalty
                                                                                                                                                                                                                                                                                                                                                                                                     2022C2
                                                                                                                                                                Randomization group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery sequence being compared:US-09-765-231A-58 (1-225)
Number of sequences searched:
2
Number of scores above cutoff:
2
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0 0 x
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    identical
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                                                    residues:
sequences searched:
scores above cutoff:
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   sequence
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0.33
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  the
                                                                                                                                             SEARCH STATISTICS
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                 initial score.
query sequence was not found
                                                                                                                                                                                        K-tuple
Joining penalty
Window size
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118
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2
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                   score.
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                                                                                       Total Elapsed 00:00:00:00.00
                                                                                                                  Standard Deviation 31.11
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The list of best scores is:

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Initial Score - Residue Identity - Gaps
                                                                                                                                                                                                                              Initial Score
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aa502552 TOIG of: aa5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence Name
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
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KEYWORDS
                                                                                                                                                                                                                                                                                                          BASE COUNT
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DEFINITION
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JOURNAL

    aa502552
    a1247782

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                         Length: 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 310.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Me Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA502552 341 bp mRNA ng62e06.s1 NCI_CGAP_Lip2 Homo sapiens cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   www-b10.llnl.gov/bbrp/image/image.html
Insert Length: 1183 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                        112
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TOIG of: a1247782
                                                                                                                                                                                                                                                                                                   /note="Vector: pAMP10; mRNA made from liposarcoma, cDNA made by oligo-dT priming. Non- directionally cloned. Size-selected on agarose gel, average insert size 600 bp Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:939394"
/clone_lib="NCI_CGAP_Lip2"
/tlssue_type="liposarcoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            'db_xref-"taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism-"Homo sapiens"
                                                                                                                                                                                                                                                 October 1, 2002 12:36 Type: N Check: 4648
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                                                                                                                                                                                         Optimized Score = 208
Matches = 209
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Eutelo Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   check:
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654
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117
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Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing Center information can be
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Initial Score **
Residue Identity **
Gaps
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AUTHORS
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ORGANISM
                                                                                                                                                                                                                                                         BASE COUNT
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60 70 80 90 100 110 120 230
CTATATTGGTTTTACCTTCAGAAGAATATTTAGTTTCACTCAGGTTTTTCAAAGCTACGCTGTCCCCCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||||||||
TTTTTTTTTTTGGCCTGCAAATAACAGAAAACTGATTACCGGTGTAGGAGATAAAGTGAT
710 V 770 230 240 250 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
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                                                                                                                                                                                    Length: 324 October 1, 2002 12:37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the TMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 821 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 324)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alia/182 324 bp mRNA linear EST 01-DEC:
qh61a07.x1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA
clone IMAGE:1849140 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: -400P from Gibco
High quality sequence stop: 317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
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                                                                                                                                                                                                                                                         105
                                                                                                                                                                                                                                      /dev_stage="20 week-post conception fetus"
//dev_stage="20 week-post conception fetus"
//lab_host="DH10B (ampicillin resistant)"
//note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
//note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
//note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
//note="Organ: Liver and Spleen; Vector: Library
//note="Organ: Spleen I; Site_2: Eco RI;
//note="Organ: Spleen I; Site_2: Eco RI;
//note="Organ: Library and Spleen I; Site_2: Eco RI;
//note="Organ: Library and Spleen I; Site_2: Eco RI adaptors
//note="Organ: Library and Eco RI Sites of the modified pT7T3 vector: Library constructed by Bento Soares and M.Fatima Bonaldo."

05 a 64 c 50 g 105 t
                                                                                                                           117
100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1849140"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
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                                                                                                 Conservative Substitutions
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Primates;
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                                                                                                                                                                                  Type: N Check: 6549
                                                                                                                       117
117
                                                                                                                Significance - Mismatches -
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6
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